

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Kraus, Matthias H.
Aaronson, Stuart A.
- (ii) TITLE OF INVENTION: AN ISOLATED POLYPEPTIDE RELATED TO THE
EPIDERMAL GROWTH FACTOR RECEPTOR, ANTIGEN THERETO, AND
BIOASSAYS AND METHODS RELATED THERETO
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Suite 400
 - (B) STREET: 133 Carnegie Way, N.W.
 - (C) CITY: Atlanta
 - (D) STATE: Georgia
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 30303
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/444,406
 - (B) FILING DATE: 01-DEC-1989
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Perryman, David G.
 - (B) REGISTRATION NUMBER: 33,438
 - (C) REFERENCE/DOCKET NUMBER: 1414-028
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (404) 688-0770
 - (B) TELEFAX: (404) 688-9880

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 66..221

(ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 780..855

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(ix) FEATURE:
      (A) NAME/KEY: exon
      (B) LOCATION: 1040..1185
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(ix) FEATURE:
      (A) NAME/KEY: intron
      (B) LOCATION: 222..779
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(ix) FEATURE:
      (A) NAME/KEY: intron
      (B) LOCATION: 856..1039
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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: join(66..221, 780..855, 1040..1185)
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTC CAGA TCTCAGTGAC TGATTCCCC AACCTTAAGA ATACTTTCTT CCCCTATAACC 60

TACAG GGA ATG TAC TAC CTT GAG GAA CAT GGT ATG GTG CAT AGA AAC 107
Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn
1 5 10

CTG GCT GCC CGA AAC GTG CTA CTC AAG TCA CCC AGT CAG GTT CAG GTG 155
Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val
15 20 25 30

GCA GAT TTT GGT GTG GCT GAC CTG CTG CCT CCT GAT GAT AAG CAG CTG 203
Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu
35 40 45

CTA TAC AGT GAG GCC AAG GTGAGGAGAC ACAAAGGGTA AGGAGGCGGG 251
Leu Tyr Ser Glu Ala Lys
50

GGTGGAGTGA AGCATGGGGA TAGGGAGCAG CCAGTGGTCT CTTCCAGAGG CAAGCAGATG 311

CTTCATGGTA AGTTCAAGGA GAGAAGGCTG CAGATGCCAG ATATTTTAGT TCAGAGGGCA 371

ACAAAGAAAA TAATGATCAA GAACTTGGGA CTGGCCGGGC GCGGTGGCTC ACGCCTGTAA 431

TCCCAACACT TCGGGAGGCC AAGGCGGGTG GATCACAAGG TCAGGAGATC AAGACCATCC 491

TGGCTAGCAC GGTGAAACCC CGTCTCTACT AAATATACAA AAAAAAAAAA ATTAGCCAGG 551

CGTGGCGGCA TGCATCTGTA CTCCCAGCTA CTCGGGAGGC TGAGGCAGGA GAATGGCGTG 611

AACCCAGGAG GCGGAGCTTG CAGTGGGCCG AGATCGCACC ACTGCACTCC AGTCTGGGCG	671
ACAGAGCGAG ACTCCGTCTC AAAAAAAAAA AAAAAAGAAT TTGGGACTTG GAAATCCTAA	731
GAAAATTTGT GGAAATAAAC TTGTGATACC TCTATCTTTA ATCCGCAG ACT CCA ATT Thr Pro Ile 55	788
AAG TGG ATG GCC CTT GAG AGT ATC CAC TTT GGG AAA TAC ACA CAC CAG Lys Trp Met Ala Leu Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln 60 65 70	836
AGT GAT GTC TGG AGC TAT G GTCAGTGCAT CTGGATGCCC TCTCTACCAT Ser Asp Val Trp Ser Tyr 75	885
CACTGGCCCC AGTTTCAAAT TTACCTTTTG AGAGCCCCCT CTTAGAATCT CTAAGCACTT	945
CAGATTTTTG TGTTAGATCA GGTTCCTGCCT TCCCTTCACT TCATGCCCAT GTCTACTATT	1005
TTGCCAGTGA CTAGTCCATG TCTTCCTGCA ACAG GT GTG ACA GTT TGG GAG Gly Val Thr Val Trp Glu 80	1056
TTG ATG ACC TTC GGG GCA GAG CCC TAT GCA GGG CTA CGA TTG GCT GAA Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg Leu Ala Glu 85 90 95	1104
GTA CCA GAC CTG CTA GAG AAG GGG GAG CGG TTG GCA CAG CCC CAG ATC Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln Pro Gln Ile 100 105 110 115	1152
TGC ACA ATT GAT GTC TAC ATG GTG ATG GTC AAG TGTGAGTTAC CTGCTGAGCC Cys Thr Ile Asp Val Tyr Met Val Met Val Lys 120 125	1205
CAACCATTTT CTCTTTTTTT CTTTTTTTTT CTTTTTTTTT TTTTTTTGAG ACAGAGTCTC	1265
ACAATTGTCA CCCAGGCTGG AGTGCAATGG TGCAATCAAT CTTGGCTCAC TACAACCTCC	1325
GCCTCTCGGG TTCAAGAGAT TCTCCTGCTT CAGCTCCGGA GTAGCTGGGA TTACAGCGCC	1385
CGCCACACCT GGATAACTGT TACACTTTTA GTAGAGATGG GGTTTCACCA TGTTGGCCAG	1445
GCTGGTCTCA AACTCCTGAC CTCAGGTGAT CCGCCTGCCT CAGCTTCCCA AAGTGCTGGG	1505
ATTACAGGTG TGAGCCATCA TGCTCGCCTG ACTGCAG	1542

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala
 1           5           10           15
Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp
          20           25           30
Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr
          35           40           45
Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His
          50           55           60
Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
          65           70           75           80
Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg
          85           90           95
Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln
          100          105          110
Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys
          115          120          125

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4905 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 100..4125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ACCAATTCGC CAGCGGTTCA GGTGGCTCTT GCCTCGATGT CCTAGCCTAG GGGCCCCCGG      60
GCCGGACTTG GCTGGGCTCC CTCACCCTC TCGGAGTC ATG AGG GCG AAC GAC      114
                               Met Arg Ala Asn Asp
                               1           5
GCT CTG CAG GTG CTG GGC TTG CTT TTC AGC CTG GCC CGG GGC TCC GAG      162
Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu Ala Arg Gly Ser Glu
          10           15           20

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GTG	GGC	AAC	TCT	CAG	GCA	GTG	TGT	CCT	GGG	ACT	CTG	AAT	GGC	CTG	AGT	210
Val	Gly	Asn	Ser	Gln	Ala	Val	Cys	Pro	Gly	Thr	Leu	Asn	Gly	Leu	Ser	
			25					30					35			
GTG	ACC	GGC	GAT	GCT	GAG	AAC	CAA	TAC	CAG	ACA	CTG	TAC	AAG	CTC	TAC	258
Val	Thr	Gly	Asp	Ala	Glu	Asn	Gln	Tyr	Gln	Thr	Leu	Tyr	Lys	Leu	Tyr	
		40					45					50				
GAG	AGG	TGT	GAG	GTG	GTG	ATG	GGG	AAC	CTT	GAG	ATT	GTG	CTC	ACG	GGA	306
Glu	Arg	Cys	Glu	Val	Val	Met	Gly	Asn	Leu	Glu	Ile	Val	Leu	Thr	Gly	
	55					60					65					
CAC	AAT	GCC	GAC	CTC	TCC	TTC	CTG	CAG	TGG	ATT	CGA	GAA	GTG	ACA	GGC	354
His	Asn	Ala	Asp	Leu	Ser	Phe	Leu	Gln	Trp	Ile	Arg	Glu	Val	Thr	Gly	
	70				75					80					85	
TAT	GTC	CTC	GTG	GCC	ATG	AAT	GAA	TTC	TCT	ACT	CTA	CCA	TTG	CCC	AAC	402
Tyr	Val	Leu	Val	Ala	Met	Asn	Glu	Phe	Ser	Thr	Leu	Pro	Leu	Pro	Asn	
				90					95					100		
CTC	CGC	GTG	GTG	CGA	GGG	ACC	CAG	GTC	TAC	GAT	GGG	AAG	TTT	GCC	ATC	450
Leu	Arg	Val	Val	Arg	Gly	Thr	Gln	Val	Tyr	Asp	Gly	Lys	Phe	Ala	Ile	
			105					110					115			
TTC	GTC	ATG	TTG	AAC	TAT	AAC	ACC	AAC	TCC	AGC	CAC	GCT	CTG	CGC	CAG	498
Phe	Val	Met	Leu	Asn	Tyr	Asn	Thr	Asn	Ser	Ser	His	Ala	Leu	Arg	Gln	
		120					125					130				
CTC	CGC	TTG	ACT	CAG	CTC	ACC	GAG	ATT	CTG	TCA	GGG	GGT	GTT	TAT	ATT	546
Leu	Arg	Leu	Thr	Gln	Leu	Thr	Glu	Ile	Leu	Ser	Gly	Gly	Val	Tyr	Ile	
	135					140					145					
GAG	AAG	AAC	GAT	AAG	CTT	TGT	CAC	ATG	GAC	ACA	ATT	GAC	TGG	AGG	GAC	594
Glu	Lys	Asn	Asp	Lys	Leu	Cys	His	Met	Asp	Thr	Ile	Asp	Trp	Arg	Asp	
	150				155					160					165	
ATC	GTG	AGG	GAC	CGA	GAT	GCT	GAG	ATA	GTG	GTG	AAG	GAC	AAT	GGC	AGA	642
Ile	Val	Arg	Asp	Arg	Asp	Ala	Glu	Ile	Val	Val	Lys	Asp	Asn	Gly	Arg	
				170				175						180		
AGC	TGT	CCC	CCC	TGT	CAT	GAG	GTT	TGC	AAG	GGG	CGA	TGC	TGG	GGT	CCT	690
Ser	Cys	Pro	Pro	Cys	His	Glu	Val	Cys	Lys	Gly	Arg	Cys	Trp	Gly	Pro	
			185					190					195			
GGA	TCA	GAA	GAC	TGC	CAG	ACA	TTG	ACC	AAG	ACC	ATC	TGT	GCT	CCT	CAG	738
Gly	Ser	Glu	Asp	Cys	Gln	Thr	Leu	Thr	Lys	Thr	Ile	Cys	Ala	Pro	Gln	
		200					205					210				
TGT	AAT	GGT	CAC	TGC	TTT	GGG	CCC	AAC	CCC	AAC	CAG	TGC	TGC	CAT	GAT	786
Cys	Asn	Gly	His	Cys	Phe	Gly	Pro	Asn	Pro	Asn	Gln	Cys	Cys	His	Asp	
	215					220					225					
GAG	TGT	GCC	GGG	GGC	TGC	TCA	GGC	CCT	CAG	GAC	ACA	GAC	TGC	TTT	GCC	834
Glu	Cys	Ala	Gly	Gly	Cys	Ser	Gly	Pro	Gln	Asp	Thr	Asp	Cys	Phe	Ala	
	230				235					240					245	

TGC Cys	CGG Arg	CAC His	TTC Phe	AAT Asn 250	GAC Asp	AGT Ser	GGA Gly	GCC Ala	TGT Cys 255	GTA Val	CCT Pro	CGC Arg	TGT Cys	CCA Pro 260	CAG Gln	882
CCT Pro	CTT Leu	GTC Val	TAC Tyr 265	AAC Asn	AAG Lys	CTA Leu	ACT Thr	TTC Phe 270	CAG Gln	CTG Leu	GAA Glu	CCC Pro	AAT Asn 275	CCC Pro	CAC His	930
ACC Thr	AAG Lys	TAT Tyr 280	CAG Gln	TAT Tyr	GGA Gly	GGA Gly	GTT Val 285	TGT Cys	GTA Val	GCC Ala	AGC Ser	TGT Cys 290	CCC Pro	CAT His	AAC Asn	978
TTT Phe	GTG Val 295	GTG Val	GAT Asp	CAA Gln	ACA Thr	TCC Ser 300	TGT Cys	GTC Val	AGG Arg	GCC Ala	TGT Cys 305	CCT Pro	CCT Pro	GAC Asp	AAG Lys	1026
ATG Met 310	GAA Glu	GTA Val	GAT Asp	AAA Lys	AAT Asn 315	GGG Gly	CTC Leu	AAG Lys	ATG Met	TGT Cys 320	GAG Glu	CCT Pro	TGT Cys	GGG Gly	GGA Gly 325	1074
CTA Leu	TGT Cys	CCC Pro	AAA Lys	GCC Ala 330	TGT Cys	GAG Glu	GGA Gly	ACA Thr	GGC Gly 335	TCT Ser	GGG Gly	AGC Ser	CGC Arg	TTC Phe 340	CAG Gln	1122
ACT Thr	GTG Val	GAC Asp	TCG Ser 345	AGC Ser	AAC Asn	ATT Ile	GAT Asp	GGA Gly 350	TTT Phe	GTG Val	AAC Asn	TGC Cys	ACC Thr 355	AAG Lys	ATC Ile	1170
CTG Leu	GGC Gly	AAC Asn 360	CTG Leu	GAC Asp	TTT Phe	CTG Leu 365	ATC Ile	ACC Thr	GGC Gly	CTC Leu	AAT Asn 370	GGA Gly	GAC Asp	CCC Pro	TGG Trp	1218
CAC His	AAG Lys 375	ATC Ile	CCT Pro	GCC Ala	CTG Leu	GAC Asp 380	CCA Pro	GAG Glu	AAG Lys	CTC Leu	AAT Asn 385	GTC Val	TTC Phe	CGG Arg	ACA Thr	1266
GTA Val 390	CGG Arg	GAG Glu	ATC Ile	ACA Thr	GGT Gly 395	TAC Tyr	CTG Leu	AAC Asn	ATC Ile 400	CAG Gln	TCC Ser	TGG Trp	CCG Pro	CCC Pro	CAC His 405	1314
ATG Met	CAC His	AAC Asn	TTC Phe	AGT Ser 410	GTT Val	TTT Phe	TCC Ser	AAT Asn	TTG Leu 415	ACA Thr	ACC Thr	ATT Ile	GGA Gly	GGC Gly 420	AGA Arg	1362
AGC Ser	CTC Leu	TAC Tyr	AAC Asn 425	CGG Arg	GGC Gly	TTC Phe	TCA Ser	TTG Leu 430	TTG Leu	ATC Ile	ATG Met	AAG Lys	AAC Asn 435	TTG Leu	AAT Asn	1410
GTC Val	ACA Thr 440	TCT Ser	CTG Leu	GGC Gly	TTC Phe	CGA Arg	TCC Ser 445	CTG Leu	AAG Lys	GAA Glu	ATT Ile	AGT Ser 450	GCT Ala	GGG Gly	CGT Arg	1458
ATC Ile 455	TAT Tyr	ATA Ile	AGT Ser	GCC Ala	AAT Asn	AGG Arg 460	CAG Gln	CTC Leu	TGC Cys	TAC Tyr	CAC His 465	CAC His	TCT Ser	TTG Leu	AAC Asn	1506

TGG Trp 470	ACC Thr	AAG Lys	GTG Val	CTT Leu	CGG Arg 475	GGG Gly	CCT Pro	ACG Thr	GAA Glu 480	GAG Glu 480	CGA Arg	CTA Leu	GAC Asp	ATC Ile	AAG Lys 485	1554
CAT His	AAT Asn	CGG Arg	CCG Pro	CGC Arg 490	AGA Arg	GAC Asp	TGC Cys	GTG Val	GCA Ala 495	GAG Glu	GGC Gly	AAA Lys	GTG Val	TGT Cys 500	GAC Asp	1602
CCA Pro	CTG Leu	TGC Cys	TCC Ser 505	TCT Ser	GGG Gly	GGA Gly	TGC Cys	TGG Trp 510	GGC Gly	CCA Pro	GGC Gly	CCT Pro	GGT Gly 515	CAG Gln	TGC Cys	1650
TTG Leu	TCC Ser	TGT Cys 520	CGA Arg	AAT Asn	TAT Tyr	AGC Ser	CGA Arg 525	GGA Gly	GGT Gly	GTC Val	TGT Cys	GTG Val 530	ACC Thr	CAC His	TGC Cys	1698
AAC Asn 535	TTT Phe	CTG Leu	AAT Asn	GGG Gly	GAG Glu	CCT Pro 540	CGA Arg	GAA Glu	TTT Phe	GCC Ala 545	CAT His	GAG Glu	GCC Ala	GAA Glu	TGC Cys	1746
TTC Phe 550	TCC Ser	TGC Cys	CAC His	CCG Pro	GAA Glu 555	TGC Cys	CAA Gln	CCC Pro	ATG Met	GAG Glu 560	GGC Gly	ACT Thr	GCC Ala	ACA Thr	TGC Cys 565	1794
AAT Asn	GGC Gly	TCG Ser	GGC Gly	TCT Ser 570	GAT Asp	ACT Thr	TGT Cys	GCT Ala	CAA Gln 575	TGT Cys	GCC Ala	CAT His	TTT Phe	CGA Arg 580	GAT Asp	1842
GGG Gly	CCC Pro	CAC His	TGT Cys 585	GTG Val	AGC Ser	AGC Ser	TGC Cys	CCC Pro 590	CAT His	GGA Gly	GTC Val	CTA Leu	GGT Gly 595	GCC Ala	AAG Lys	1890
GGC Gly	CCA Pro	ATC Ile 600	TAC Tyr	AAG Lys	TAC Tyr	CCA Pro	GAT Asp 605	GTT Val	CAG Gln	AAT Asn	GAA Glu	TGT Cys 610	CGG Arg	CCC Pro	TGC Cys	1938
CAT His 615	GAG Glu	AAC Asn	TGC Cys	ACC Thr	CAG Gln	GGG Gly 620	TGT Cys	AAA Lys	GGA Gly	CCA Pro	GAG Glu 625	CTT Leu	CAA Gln	GAC Asp	TGT Cys	1986
TTA Leu 630	GGA Gly	CAA Gln	ACA Thr	CTG Leu	GTG Val 635	CTG Leu	ATC Ile	GGC Gly	AAA Lys	ACC Thr 640	CAT His	CTG Leu	ACA Thr	ATG Met	GCT Ala 645	2034
TTG Leu	ACA Thr	GTG Val	ATA Ile	GCA Ala 650	GGA Gly	TTG Leu	GTA Val	GTG Val	ATT Ile 655	TTC Phe	ATG Met	ATG Met	CTG Leu	GGC Gly 660	GGC Gly	2082
ACT Thr	TTT Phe	CTC Leu	TAC Tyr 665	TGG Trp	CGT Arg	GGG Gly	CGC Arg	CGG Arg 670	ATT Ile	CAG Gln	AAT Asn	AAA Lys	AGG Arg 675	GCT Ala	ATG Met	2130
AGG Arg	CGA Arg	TAC Tyr 680	TTG Leu	GAA Glu	CGG Arg	GGT Gly	GAG Glu 685	AGC Ser	ATA Ile	GAG Glu	CCT Pro	CTG Leu 690	GAC Asp	CCC Pro	AGT Ser	2178

GAG Glu	AAG Lys	GCT Ala	AAC Asn	AAA Lys	GTC Val	TTG Leu	GCC Ala	AGA Arg	ATC Ile	TTC Phe	AAA Lys	GAG Glu	ACA Thr	GAG Glu	CTA Leu	2226
695						700					705					
AGG Arg	AAG Lys	CTT Leu	AAA Lys	GTG Val	CTT Leu	GGC Gly	TCG Ser	GGT Gly	GTC Val	TTT Phe	GGA Gly	ACT Thr	GTG Val	CAC His	AAA Lys	2274
710					715					720					725	
GGA Gly	GTG Val	TGG Trp	ATC Ile	CCT Pro	GAG Glu	GGT Gly	GAA Glu	TCA Ser	ATC Ile	AAG Lys	ATT Ile	CCA Pro	GTC Val	TGC Cys	ATT Ile	2322
				730					735					740		
AAA Lys	GTC Val	ATT Ile	GAG Glu	GAC Asp	AAG Lys	AGT Ser	GGA Gly	CGG Arg	CAG Gln	AGT Ser	TTT Phe	CAA Gln	GCT Ala	GTG Val	ACA Thr	2370
			745					750				755				
GAT Asp	CAT His	ATG Met	CTG Leu	GCC Ala	ATT Ile	GGC Gly	AGC Ser	CTG Leu	GAC Asp	CAT His	GCC Ala	CAC His	ATT Ile	GTA Val	AGG Arg	2418
		760					765				770					
CTG Leu	CTG Leu	GGA Gly	CTA Leu	TGC Cys	CCA Pro	GGG Gly	TCA Ser	TCT Ser	CTG Leu	CAG Gln	CTT Leu	GTC Val	ACT Thr	CAA Gln	TAT Tyr	2466
	775					780					785					
TTG Leu	CCT Pro	CTG Leu	GGT Gly	TCT Ser	CTG Leu	CTG Leu	GAT Asp	CAT His	GTG Val	AGA Arg	CAA Gln	CAC His	CGG Arg	GGG Gly	GCA Ala	2514
790					795					800					805	
CTG Leu	GGG Gly	CCA Pro	CAG Gln	CTG Leu	CTG Leu	CTC Leu	AAC Asn	TGG Trp	GGA Gly	GTA Val	CAA Gln	ATT Ile	GCC Ala	AAG Lys	GGA Gly	2562
			810						815					820		
ATG Met	TAC Tyr	TAC Tyr	CTT Leu	GAG Glu	GAA Glu	CAT His	GGT Gly	ATG Met	GTG Val	CAT His	AGA Arg	AAC Asn	CTG Leu	GCT Ala	GCC Ala	2610
			825					830					835			
CGA Arg	AAC Asn	GTG Val	CTA Leu	CTC Leu	AAG Lys	TCA Ser	CCC Pro	AGT Ser	CAG Gln	GTT Val	CAG Gln	GTG Val	GCA Ala	GAT Asp	TTT Phe	2658
		840					845					850				
GGT Gly	GTG Val	GCT Ala	GAC Asp	CTG Leu	CTG Leu	CCT Pro	CCT Pro	GAT Asp	GAT Asp	AAG Lys	CAG Gln	CTG Leu	CTA Leu	TAC Tyr	AGT Ser	2706
	855					860					865					
GAG Glu	GCC Ala	AAG Lys	ACT Thr	CCA Pro	ATT Ile	AAG Lys	TGG Trp	ATG Met	GCC Ala	CTT Leu	GAG Glu	AGT Ser	ATC Ile	CAC His	TTT Phe	2754
870					875				880						885	
GGG Gly	AAA Lys	TAC Tyr	ACA Thr	CAC His	CAG Gln	AGT Ser	GAT Asp	GTC Val	TGG Trp	AGC Ser	TAT Tyr	GGT Gly	GTG Val	ACA Thr	GTT Val	2802
				890					895					900		
TGG Trp	GAG Glu	TTG Leu	ATG Met	ACC Thr	TTC Phe	GGG Gly	GCA Ala	GAG Glu	CCC Pro	TAT Tyr	GCA Ala	GGG Gly	CTA Leu	CGA Arg	TTG Leu	2850
			905					910					915			

GCT Ala	GAA Glu	GTA Val 920	CCA Pro	GAC Asp	CTG Leu	CTA Leu	GAG Glu 925	AAG Lys	GGG Gly	GAG Glu	CGG Arg	TTG Leu 930	GCA Ala	CAG Gln	CCC Pro	2898
CAG Gln 935	ATC Ile	TGC Cys	ACA Thr	ATT Ile	GAT Asp	GTC Val 940	TAC Tyr	ATG Met	GTG Val	ATG Met	GTC Val 945	AAG Lys	TGT Cys	TGG Trp	ATG Met	2946
ATT Ile 950	GAT Asp	GAG Glu	AAC Asn	ATT Ile	CGC Arg 955	CCA Pro	ACC Thr	TTT Phe	AAA Lys	GAA Glu 960	CTA Leu	GCC Ala	AAT Asn	GAG Glu	TTC Phe 965	2994
ACC Thr	AGG Arg	ATG Met	GCC Ala	CGA Arg 970	GAC Asp	CCA Pro	CCA Pro	CGG Arg	TAT Tyr 975	CTG Leu	GTC Val	ATA Ile	AAG Lys	AGA Arg 980	GAG Glu	3042
AGT Ser	GGG Gly	CCT Pro	GGA Gly 985	ATA Ile	GCC Ala	CCT Pro	GGG Gly	CCA Pro 990	GAG Glu	CCC Pro	CAT His	GGT Gly	CTG Leu 995	ACA Thr	AAC Asn	3090
AAG Lys	AAG Lys	CTA Leu 1000	GAG Glu	GAA Glu	GTA Val	GAG Glu	CTG Leu 1005	GAG Glu	CCA Pro	GAA Glu	CTA Leu	GAC Asp 1010	CTA Leu	GAC Asp	CTA Leu	3138
GAC Asp 1015	TTG Leu	GAA Glu	GCA Ala	GAG Glu	GAG Glu	GAC Asp	AAC Asn	CTG Leu 1020	GCA Ala	ACC Thr	ACC Thr	ACA Thr	CTG Leu	GGC Gly	TCC Ser	3186
GCC Ala 1030	CTC Leu	AGC Ser	CTA Leu	CCA Pro	GTT Val 1035	GGA Gly	ACA Thr	CTT Leu	AAT Asn	CGG Arg 1040	CCA Pro	CGT Arg	GGG Gly	AGC Ser	CAG Gln 1045	3234
AGC Ser	CTT Leu	TTA Leu	AGT Ser	CCA Pro 1050	TCA Ser	TCT Ser	GGA Gly	TAC Tyr	ATG Met	CCC Pro 1055	ATG Met	AAC Asn	CAG Gln	GGT Gly	AAT Asn 1060	3282
CTT Leu	GGG Gly	GAG Glu	TCT Ser 1065	TGC Cys	CAG Gln	GAG Glu	TCT Ser	GCA Ala 1070	GTT Val	TCT Ser	GGG Gly	AGC Ser	AGT Ser	GAA Glu	CGG Arg	3330
TGC Cys	CCC Pro	CGT Arg 1080	CCA Pro	GTC Val	TCT Ser	CTA Leu	CAC His 1085	CCA Pro	ATG Met	CCA Pro	CGG Arg	GGA Gly 1090	TGC Cys	CTG Leu	GCA Ala	3378
TCA Ser 1095	GAG Glu	TCA Ser	TCA Ser	GAG Glu	GGG Gly	CAT His 1100	GTA Val	ACA Thr	GGC Gly	TCT Ser	GAG Glu 1105	GCT Ala	GAG Glu	CTC Leu	CAG Gln	3426
GAG Glu 1110	AAA Lys	GTG Val	TCA Ser	ATG Met	TGT Cys 1115	AGA Arg	AGC Ser	CGG Arg	AGC Ser	AGG Arg 1120	AGC Ser	CGG Arg	AGC Ser	CCA Pro	CGG Arg 1125	3474
CCA Pro	CGC Arg	GGA Gly	GAT Asp	AGC Ser 1130	GCC Ala	TAC Tyr	CAT His	TCC Ser	CAG Gln 1135	CGC Arg	CAC His	AGT Ser	CTG Leu	CTG Leu	ACT Thr 1140	3522

CCT GTT ACC CCA CTC TCC CCA CCC GGG TTA GAG GAA GAG GAT GTC AAC Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu Glu Glu Asp Val Asn 1145 1150 1155	3570
GGT TAT GTC ATG CCA GAT ACA CAC CTC AAA GGT ACT CCC TCC TCC CGG Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly Thr Pro Ser Ser Arg 1160 1165 1170	3618
GAA GGC ACC CTT TCT TCA GTG GGT CTT AGT TCT GTC CTG GGT ACT GAA Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser Val Leu Gly Thr Glu 1175 1180 1185	3666
GAA GAA GAT GAA GAT GAG GAG TAT GAA TAC ATG AAC CGG AGG AGA AGG Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg 1190 1195 1200 1205	3714
CAC AGT CCA CCT CAT CCC CCT AGG CCA AGT TCC CTT GAG GAG CTG GGT His Ser Pro Pro His Pro Pro Arg Pro Ser Ser Leu Glu Glu Leu Gly 1210 1215 1220	3762
TAT GAG TAC ATG GAT GTG GGG TCA GAC CTC AGT GCC TCT CTG GGC AGC Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser Ala Ser Leu Gly Ser 1225 1230 1235	3810
ACA CAG AGT TGC CCA CTC CAC CCT GTA CCC ATC ATG CCC ACT GCA GGC Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile Met Pro Thr Ala Gly 1240 1245 1250	3858
ACA ACT CCA GAT GAA GAC TAT GAA TAT ATG AAT CGG CAA CGA GAT GGA Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp Gly 1255 1260 1265	3906
GGT GGT CCT GGG GGT GAT TAT GCA GCC ATG GGG GCC TGC CCA GCA TCT Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly Ala Cys Pro Ala Ser 1270 1275 1280 1285	3954
GAG CAA GGG TAT GAA GAG ATG AGA GCT TTT CAG GGG CCT GGA CAT CAG Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln Gly Pro Gly His Gln 1290 1295 1300	4002
GCC CCC CAT GTC CAT TAT GCC CGC CTA AAA ACT CTA CGT AGC TTA GAG Ala Pro His Val His Tyr Ala Arg Leu Lys Thr Leu Arg Ser Leu Glu 1305 1310 1315	4050
GCT ACA GAC TCT GCC TTT GAT AAC CCT GAT TAC TGG CAT AGC AGG CTT Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr Trp His Ser Arg Leu 1320 1325 1330	4098
TTC CCC AAG GCT AAT GCC CAG AGA ACG TAACTCCTGC TCCCTGTGGC Phe Pro Lys Ala Asn Ala Gln Arg Thr 1335 1340	4145
ACTCAGGGAG CATTTAATGG CAGCTAGTGC CTTTAGAGGG TACCGTCTTC TCCCTATTCC	4205
CTCTCTCTCC CAGGTCCCAG CCCCTTTTCC CCAGTCCCAG ACAATTCCAT TCAATCTTG	4265

GAGGCTTTTA AACATTTTGA CACAAAATTC TTATGGTATG TAGCCAGCTG TGCACTTTCT 4325
 TCTCTTTCCC AACCCCAGGA AAGGTTTTCC TTATTTTGTG TGCTTTCCCA GTCCCATTCC 4385
 TCAGCTTCTT CACAGGCACT CCTGGAGATA TGAAGGATTA CTCTCCATAT CCCTTCCTCT 4445
 CAGGCTCTTG ACTACTTGGA ACTAGGCTCT TATGTGTGCC TTTGTTTCCC ATCAGACTGT 4505
 CAAGAAGAGG AAAGGGAGGA AACCTAGCAG AGGAAAGTGT AATTTTGGTT TATGACTCTT 4565
 AACCCCCTAG AAAGACAGAA GCTTAAATC TGTGAAGAAA GAGGTTAGGA GTAGATATTG 4625
 ATTACTATCA TAATTCAGCA CTTAACTATG AGCCAGGCAT CATACTAAAC TTCACCTACA 4685
 TTATCTCACT TAGTCCTTTA TCATCCTTAA AACAATTCTG TGACATACAT ATTATCTCAT 4745
 TTTACACAAA GGAAGTCGG GCATGGTGGC TCATGCCTGT AATCTCAGCA CTTTGGGAGG 4805
 CTGAGGCAGA AGGATTACCT GAGGCAAGGA GTTTGAGACC AGCTTAGCCA ACATAGTAAG 4865
 ACCCCCATCT CTTTAAAAAA AAAAAAAAAA AAAAAAAAAA 4905

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
 1 5 10 15
 Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
 20 25 30
 Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
 35 40 45
 Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
 50 55 60
 Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
 65 70 75 80
 Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
 85 90 95
 Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
 100 105 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
 115 120 125
 His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
 130 135 140
 Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
 145 150 155 160
 Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
 165 170 175
 Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
 180 185 190
 Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
 195 200 205
 Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
 210 215 220
 Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
 225 230 235 240
 Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
 245 250 255
 Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
 260 265 270
 Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
 275 280 285
 Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
 290 295 300
 Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
 305 310 315 320
 Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
 325 330 335
 Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
 340 345 350
 Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
 355 360 365
 Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
 370 375 380
 Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
 385 390 395 400

Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
 405 410 415
 Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
 420 425 430
 Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
 435 440 445
 Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
 450 455 460
 His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
 465 470 475 480
 Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
 485 490 495
 Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
 500 505 510
 Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
 515 520 525
 Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
 530 535 540
 His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
 545 550 555 560
 Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
 565 570 575
 Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
 580 585 590
 Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
 595 600 605
 Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
 610 615 620
 Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
 625 630 635 640
 His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
 645 650 655
 Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
 660 665 670
 Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
 675 680 685

Pro	Leu	Asp	Pro	Ser	Glu	Lys	Ala	Asn	Lys	Val	Leu	Ala	Arg	Ile	Phe
690						695					700				
Lys	Glu	Thr	Glu	Leu	Arg	Lys	Leu	Lys	Val	Leu	Gly	Ser	Gly	Val	Phe
705					710					715					720
Gly	Thr	Val	His	Lys	Gly	Val	Trp	Ile	Pro	Glu	Gly	Glu	Ser	Ile	Lys
				725					730					735	
Ile	Pro	Val	Cys	Ile	Lys	Val	Ile	Glu	Asp	Lys	Ser	Gly	Arg	Gln	Ser
			740					745					750		
Phe	Gln	Ala	Val	Thr	Asp	His	Met	Leu	Ala	Ile	Gly	Ser	Leu	Asp	His
		755					760					765			
Ala	His	Ile	Val	Arg	Leu	Leu	Gly	Leu	Cys	Pro	Gly	Ser	Ser	Leu	Gln
		770				775					780				
Leu	Val	Thr	Gln	Tyr	Leu	Pro	Leu	Gly	Ser	Leu	Leu	Asp	His	Val	Arg
785					790					795					800
Gln	His	Arg	Gly	Ala	Leu	Gly	Pro	Gln	Leu	Leu	Leu	Asn	Trp	Gly	Val
				805					810					815	
Gln	Ile	Ala	Lys	Gly	Met	Tyr	Tyr	Leu	Glu	Glu	His	Gly	Met	Val	His
			820					825					830		
Arg	Asn	Leu	Ala	Ala	Arg	Asn	Val	Leu	Leu	Lys	Ser	Pro	Ser	Gln	Val
		835					840					845			
Gln	Val	Ala	Asp	Phe	Gly	Val	Ala	Asp	Leu	Leu	Pro	Pro	Asp	Asp	Lys
		850				855					860				
Gln	Leu	Leu	Tyr	Ser	Glu	Ala	Lys	Thr	Pro	Ile	Lys	Trp	Met	Ala	Leu
865					870					875					880
Glu	Ser	Ile	His	Phe	Gly	Lys	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser
				885					890					895	
Tyr	Gly	Val	Thr	Val	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Glu	Pro	Tyr
			900					905					910		
Ala	Gly	Leu	Arg	Leu	Ala	Glu	Val	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu
		915					920					925			
Arg	Leu	Ala	Gln	Pro	Gln	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Val	Met
		930				935					940				
Val	Lys	Cys	Trp	Met	Ile	Asp	Glu	Asn	Ile	Arg	Pro	Thr	Phe	Lys	Glu
945					950					955					960
Leu	Ala	Asn	Glu	Phe	Thr	Arg	Met	Ala	Arg	Asp	Pro	Pro	Arg	Tyr	Leu
				965					970						975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
 980 985 990
 His Gly Leu Thr Asn Lys Lys Leu Glu Glu Val Glu Leu Glu Pro Glu
 995 1000 1005
 Leu Asp Leu Asp Leu Asp Leu Glu Ala Glu Glu Asp Asn Leu Ala Thr
 1010 1015 1020
 Thr Thr Leu Gly Ser Ala Leu Ser Leu Pro Val Gly Thr Leu Asn Arg
 1025 1030 1035 1040
 Pro Arg Gly Ser Gln Ser Leu Leu Ser Pro Ser Ser Gly Tyr Met Pro
 1045 1050 1055
 Met Asn Gln Gly Asn Leu Gly Glu Ser Cys Gln Glu Ser Ala Val Ser
 1060 1065 1070
 Gly Ser Ser Glu Arg Cys Pro Arg Pro Val Ser Leu His Pro Met Pro
 1075 1080 1085
 Arg Gly Cys Leu Ala Ser Glu Ser Ser Glu Gly His Val Thr Gly Ser
 1090 1095 1100
 Glu Ala Glu Leu Gln Glu Lys Val Ser Met Cys Arg Ser Arg Ser Arg
 1105 1110 1115 1120
 Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser Ala Tyr His Ser Gln Arg
 1125 1130 1135
 His Ser Leu Leu Thr Pro Val Thr Pro Leu Ser Pro Pro Gly Leu Glu
 1140 1145 1150
 Glu Glu Asp Val Asn Gly Tyr Val Met Pro Asp Thr His Leu Lys Gly
 1155 1160 1165
 Thr Pro Ser Ser Arg Glu Gly Thr Leu Ser Ser Val Gly Leu Ser Ser
 1170 1175 1180
 Val Leu Gly Thr Glu Glu Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met
 1185 1190 1195 1200
 Asn Arg Arg Arg Arg His Ser Pro Pro His Pro Pro Arg Pro Ser Ser
 1205 1210 1215
 Leu Glu Glu Leu Gly Tyr Glu Tyr Met Asp Val Gly Ser Asp Leu Ser
 1220 1225 1230
 Ala Ser Leu Gly Ser Thr Gln Ser Cys Pro Leu His Pro Val Pro Ile
 1235 1240 1245
 Met Pro Thr Ala Gly Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn
 1250 1255 1260

Arg Gln Arg Asp Gly Gly Gly Pro Gly Gly Asp Tyr Ala Ala Met Gly
1265 1270 1275 1280

Ala Cys Pro Ala Ser Glu Gln Gly Tyr Glu Glu Met Arg Ala Phe Gln
1285 1290 1295

Gly Pro Gly His Gln Ala Pro His Val His Tyr Ala Arg Leu Lys Thr
1300 1305 1310

Leu Arg Ser Leu Glu Ala Thr Asp Ser Ala Phe Asp Asn Pro Asp Tyr
1315 1320 1325

Trp His Ser Arg Leu Phe Pro Lys Ala Asn Ala Gln Arg Thr
1330 1335 1340

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Glu Asp Glu Asp Glu Glu Tyr Glu Tyr Met Asn Arg Arg Arg Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Thr Pro Asp Glu Asp Tyr Glu Tyr Met Asn Arg Gln Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Glu Glu Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Ser Arg Ser Arg Ser Arg Ser Pro Arg Pro Arg Gly Asp Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Tyr Met Asn Arg Arg Arg Arg His Ser Pro Pro His Pro Pro Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCTCGAGT CGAC

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCGTCGAC TCGA

14

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Glu Tyr Met Asn
1 5